

0360

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/053,410

DATE: 02/12/2002

TIME: 12:00:32

Input Set : A:\1276SEQLIST.TXT

Output Set: N:\CRF3\02122002\J053410.raw

ENTERED

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4 <110> APPLICANT: Sewalt, Vincent J. H.
5     Jung, Rudolf
6     Hu, Wang-Nan
7     Meeley, Robert B.
9 <120> TITLE OF INVENTION: Improved Grain Quality Through Altered
10    Expression of Seed Proteins
13 <130> FILE REFERENCE: 1276
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/053,410
C--> 15 <141> CURRENT FILING DATE: 2001-11-07
15 <150> PRIOR APPLICATION NUMBER: US 60/246,455
16 <151> PRIOR FILING DATE: 2000-11-07
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1129
24 <212> TYPE: DNA
25 <213> ORGANISM: Zea mays
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (120)...(1004)
30 <223> OTHER INFORMATION: 50 kD gamma-zein prolamin/PTA 2272
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33  gtgtatttgc actcatgcat cacaaaacat ccttctatca gtaccatcaa tcatcattca      60
34  tcttagtagt ataggcacca aatcaaactc gcaacatcaa ttatctaact ccaaaaacc      119
35  atg aag ctg gtg ctt gtg gtt ctt gct ttc att gct tta gta tca agt      167
36  Met Lys Leu Val Leu Val Val Leu Ala Phe Ile Ala Leu Val Ser Ser
37  1          5          10          15
39  gtt tct tgt aca cag aca ggc ggc tgc agc tgt ggt caa caa caa agc      215
40  Val Ser Cys Thr Gln Thr Gly Gly Cys Ser Cys Gly Gln Gln Gln Ser
41          20          25          30
43  cat gag cag caa cat cat cca caa caa cat cat cca caa aaa caa caa      263
44  His Glu Gln Gln His His Pro Gln Gln His His Pro Gln Lys Gln Gln
45          35          40          45
47  cat caa cca cca cca caa cat cac cag cag cag caa cac caa caa caa      311
48  His Gln Pro Pro Pro Gln His His Gln Gln Gln Gln His Gln Gln Gln
49          50          55          60
51  caa gtt cac atg caa cca caa aaa cat cag caa caa caa gaa gtt cat      359
52  Gln Val His Met Gln Pro Gln Lys His Gln Gln Gln Gln Gln Glu Val His
53  65          70          75          80
55  gtt caa caa caa caa caa ccg cag cac caa caa caa caa caa caa      407
56  Val Gln Gln Gln Gln Gln Gln Pro Gln His Gln Gln Gln Gln Gln Gln
57          85          90          95
59  caa cag cac caa caa caa cat caa tgt gaa ggc caa caa caa cat cac      455

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60  Gln Gln His Gln Gln Gln His Gln Cys Glu Gly Gln Gln Gln His His
61                100                105                110
63  caa caa tca caa ggc cat gtg caa caa cac gaa cag agc cat gag caa      503
64  Gln Gln Ser Gln Gly His Val Gln Gln His Glu Gln Ser His Glu Gln
65                115                120                125
67  cac caa gga cag agc cat gag caa caa cat caa caa caa ttc cag ggt      551
68  His Gln Gly Gln Ser His Glu Gln Gln His Gln Gln Gln Phe Gln Gly
69                130                135                140
71  cat gac aag cag caa caa cca caa cag cct cag caa tat cag cag ggc      599
72  His Asp Lys Gln Gln Gln Pro Gln Gln Pro Gln Gln Tyr Gln Gln Gly
73  145                150                155                160
75  cag gaa aaa tca caa cag caa caa tgt cat tgc cag gag cag caa cag      647
76  Gln Glu Lys Ser Gln Gln Gln Gln Cys His Cys Gln Glu Gln Gln Gln
77                165                170                175
79  act aca agg tgc agc tat aac tac tat agc agt agc tca aat cta aaa      695
80  Thr Thr Arg Cys Ser Tyr Asn Tyr Tyr Ser Ser Ser Ser Asn Leu Lys
81                180                185                190
83  aat tgt cat gaa ttc cta agg cag cag tgc agc cct ttg gta atg cct      743
84  Asn Cys His Glu Phe Leu Arg Gln Gln Cys Ser Pro Leu Val Met Pro
85                195                200                205
87  ttt ctc caa tca cgt ttg ata caa cca agt agc tgc cag gta ttg cag      791
88  Phe Leu Gln Ser Arg Leu Ile Gln Pro Ser Ser Cys Gln Val Leu Gln
89                210                215                220
91  caa caa tgt tgt cat gat ctt agg cag att gag cca caa tac att cac      839
92  Gln Gln Cys Cys His Asp Leu Arg Gln Ile Glu Pro Gln Tyr Ile His
93  225                230                235                240
95  caa gca atc tac aac atg gtt caa tcc ata atc cag gag gag caa caa      887
96  Gln Ala Ile Tyr Asn Met Val Gln Ser Ile Ile Gln Glu Glu Gln Gln
97                245                250                255
99  caa caa cca tgt gag tta tgt gga tct caa caa gct act cca aag tgc      935
100 Gln Gln Pro Cys Glu Leu Cys Gly Ser Gln Gln Ala Thr Pro Lys Cys
101                260                265                270
103 ggt ggc aat ctt gac agc agc aca ata cct acc atc aat gtg cgg ctt      983
104 Gly Gly Asn Leu Asp Ser Ser Thr Ile Pro Thr Ile Asn Val Arg Leu
105                275                280                285
107 gta cca ctc ata cta cca aaa taatccatgc agcagcaatg acattagtgg      1034
108 Val Pro Leu Ile Leu Pro Lys
109                290                295
111 tgtttgcaat tgaagaattg tgtctacctt gccgttatac tcatataacg gtgttaagca      1094
112 ataaagtacc atacattatg atgttaaaaa aaaaa      1129
114 <210> SEQ ID NO: 2
115 <211> LENGTH: 295
116 <212> TYPE: PRT
117 <213> ORGANISM: Zea mays
119 <400> SEQUENCE: 2
120 Met Lys Leu Val Leu Val Val Leu Ala Phe Ile Ala Leu Val Ser Ser
121 1 5 10 15
122 Val Ser Cys Thr Gln Thr Gly Gly Cys Ser Cys Gly Gln Gln Gln Ser
123 20 25 30

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124 His Glu Gln Gln His His Pro Gln Gln His His Pro Gln Lys Gln Gln
125          35          40          45
126 His Gln Pro Pro Pro Gln His His Gln Gln Gln Gln His Gln Gln Gln
127          50          55          60
128 Gln Val His Met Gln Pro Gln Lys His Gln Gln Gln Gln Glu Val His
129          65          70          75          80
130 Val Gln Gln Gln Gln Gln Gln Pro Gln His Gln Gln Gln Gln Gln Gln
131          85          90          95
132 Gln Gln His Gln Gln Gln His Gln Cys Glu Gly Gln Gln Gln His His
133          100          105          110
134 Gln Gln Ser Gln Gly His Val Gln Gln His Glu Gln Ser His Glu Gln
135          115          120          125
136 His Gln Gly Gln Ser His Glu Gln Gln His Gln Gln Gln Phe Gln Gly
137          130          135          140
138 His Asp Lys Gln Gln Gln Pro Gln Gln Pro Gln Gln Tyr Gln Gln Gly
139          145          150          155          160
140 Gln Glu Lys Ser Gln Gln Gln Gln Cys His Cys Gln Glu Gln Gln Gln
141          165          170          175
142 Thr Thr Arg Cys Ser Tyr Asn Tyr Tyr Ser Ser Ser Ser Asn Leu Lys
143          180          185          190
144 Asn Cys His Glu Phe Leu Arg Gln Gln Cys Ser Pro Leu Val Met Pro
145          195          200          205
146 Phe Leu Gln Ser Arg Leu Ile Gln Pro Ser Ser Cys Gln Val Leu Gln
147          210          215          220
148 Gln Gln Cys Cys His Asp Leu Arg Gln Ile Glu Pro Gln Tyr Ile His
149          225          230          235          240
150 Gln Ala Ile Tyr Asn Met Val Gln Ser Ile Ile Gln Glu Glu Gln Gln
151          245          250          255
152 Gln Gln Pro Cys Glu Leu Cys Gly Ser Gln Gln Ala Thr Pro Lys Cys
153          260          265          270
154 Gly Gly Asn Leu Asp Ser Ser Thr Ile Pro Thr Ile Asn Val Arg Leu
155          275          280          285
156 Val Pro Leu Ile Leu Pro Lys
157          290          295
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 950
161 <212> TYPE: DNA
162 <213> ORGANISM: Zea mays
164 <220> FEATURE:
165 <221> NAME/KEY: CDS
166 <222> LOCATION: (111)...(728)
167 <223> OTHER INFORMATION: 18 kD alpha-globulin/PTA 2274
169 <400> SEQUENCE: 3
170 aaaaaaaccc cctcgtcgat caccaccaa gaacacagta actagcagct agcacatcaa 60
171 acaagtggcg acagacaaag atttgtgagg gtgatccgcg ctgagaagag atg gct 116
172                                     Met Ala
173                                     1
175 aag atc gcc gcg gcg gcg gcg gcg gcg ctg tgc ttc gcg gcc ctg gtg 164
176 Lys Ile Ala Ala Ala Ala Ala Ala Ala Leu Cys Phe Ala Ala Leu Val

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177          5          10          15
179 gcc gtg gcc gtc tgc caa ggc gag gtc gag cgg cag agg ctc agg gac 212
180 Ala Val Ala Val Cys Gln Gly Glu Val Glu Arg Gln Arg Leu Arg Asp
181          20          25          30
183 ctg cag tgc tgg cag gag gtc cag gag agc ccg ctc gac gcg tgc cgc 260
184 Leu Gln Cys Trp Gln Glu Val Gln Glu Ser Pro Leu Asp Ala Cys Arg
185          35          40          45          50
187 cag gtc ctc gac cgg cag cta acc ggc ggc ggc ggc ggc ggc ggc gtt 308
188 Gln Val Leu Asp Arg Gln Leu Thr Gly Gly Gly Gly Gly Gly Gly Val
189          55          60          65
191 ggc ccg ttc cgg tgg ggc acc ggg ctc cgg atg cgg tgc tgc cag cag 356
192 Gly Pro Phe Arg Trp Gly Thr Gly Leu Arg Met Arg Cys Cys Gln Gln
193          70          75          80
195 ctc cag gac gtg agc cgc gag tgc cgc tgc gcc gcc atc cgg agc atg 404
196 Leu Gln Asp Val Ser Arg Glu Cys Arg Cys Ala Ala Ile Arg Ser Met
197          85          90          95
199 gtc agg ggc tac gag gag gcc atg ccg ccg ctg gag aaa ggc tgg tgg 452
200 Val Arg Gly Tyr Glu Glu Ala Met Pro Pro Leu Glu Lys Gly Trp Trp
201          100          105          110
203 cca tgg ggg cgg cag cag cag ccg ccg ccg cag gga gga gga gga gga 500
204 Pro Trp Gly Arg Gln Gln Gln Pro Pro Pro Gln Gly Gly Gly Gly Gly
205          115          120          125          130
207 cag ggg ggc tac tac tac ccc tgc agc cgg cca gga gag gga tac ggc 548
208 Gln Gly Gly Tyr Tyr Tyr Pro Cys Ser Arg Pro Gly Glu Gly Tyr Gly
209          135          140          145
211 tac ggt cag ggt ggc cag cgg cag atg tat cca ccg tgt cgt ccc ggc 596
212 Tyr Gly Gln Gly Gly Gln Arg Gln Met Tyr Pro Pro Cys Arg Pro Gly
213          150          155          160
215 acc acc ggc ggc ggg cca agg atc ggc cgc gtg agg ctt acg aag gcc 644
216 Thr Thr Gly Gly Gly Pro Arg Ile Gly Arg Val Arg Leu Thr Lys Ala
217          165          170          175
219 cgg gag tac gcc gcg ggg ttg ccg atg atg tgc cgg ctg tcg gag ccc 692
220 Arg Glu Tyr Ala Ala Gly Leu Pro Met Met Cys Arg Leu Ser Glu Pro
221          180          185          190
223 cag gag tgc agc atc ttc tcc ggc ggc gac cag tac tagctaccat 738
224 Gln Glu Cys Ser Ile Phe Ser Gly Gly Asp Gln Tyr
225          195          200          205
227 ggttaaagcg agtcggcgcg aggtgcaaga cgcagcatgt gtactgtgcg cgtgcaaatac 798
228 cagaatgacg tagctctgac gtgggctcgc aatattgtcg cgtgttcggtt acaataatga 858
229 taataactat gaggaataaaa tatgggaatg ttgccagata gtactggcgc cgtttcttca 918
230 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 950
232 <210> SEQ ID NO: 4
233 <211> LENGTH: 206
234 <212> TYPE: PRT
235 <213> ORGANISM: Zea mays
237 <400> SEQUENCE: 4
238 Met Ala Lys Ile Ala Ala Ala Ala Ala Ala Ala Leu Cys Phe Ala Ala
239 1 5 10 15
240 Leu Val Ala Val Ala Val Cys Gln Gly Glu Val Glu Arg Gln Arg Leu

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TIME: 12:00:32

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Output Set: N:\CRF3\02122002\J053410.raw

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241          20          25          30
242 Arg Asp Leu Gln Cys Trp Gln Glu Val Gln Glu Ser Pro Leu Asp Ala
243          35          40          45
244 Cys Arg Gln Val Leu Asp Arg Gln Leu Thr Gly Gly Gly Gly Gly Gly
245          50          55          60
246 Gly Val Gly Pro Phe Arg Trp Gly Thr Gly Leu Arg Met Arg Cys Cys
247          65          70          75          80
248 Gln Gln Leu Gln Asp Val Ser Arg Glu Cys Arg Cys Ala Ala Ile Arg
249          85          90          95
250 Ser Met Val Arg Gly Tyr Glu Glu Ala Met Pro Pro Leu Glu Lys Gly
251          100         105         110
252 Trp Trp Pro Trp Gly Arg Gln Gln Pro Pro Pro Gln Gly Gly Gly
253          115         120         125
254 Gly Gly Gln Gly Gly Tyr Tyr Tyr Pro Cys Ser Arg Pro Gly Glu Gly
255          130         135         140
256 Tyr Gly Tyr Gly Gln Gly Gly Gln Arg Gln Met Tyr Pro Pro Cys Arg
257          145         150         155         160
258 Pro Gly Thr Thr Gly Gly Gly Pro Arg Ile Gly Arg Val Arg Leu Thr
259          165         170         175
260 Lys Ala Arg Glu Tyr Ala Ala Gly Leu Pro Met Met Cys Arg Leu Ser
261          180         185         190
262 Glu Pro Gln Glu Cys Ser Ile Phe Ser Gly Gly Asp Gln Tyr
263          195         200         205
265 <210> SEQ ID NO: 5
266 <211> LENGTH: 1679
267 <212> TYPE: DNA
268 <213> ORGANISM: Zea mays
270 <220> FEATURE:
271 <221> NAME/KEY: CDS
272 <222> LOCATION: (34)...(1485)
273 <223> OTHER INFORMATION: 50 kD legumin-1 prolamin/PTA 2273
275 <400> SEQUENCE: 5
276 gcacgaggag cgagcgagca gaggcagcgc aca atg gcg gcg gca ata gta ctc          54
277                               Met Ala Ala Ala Ile Val Leu
278                               1          5
280 tcc ggc cag gtg cgg ccg ctt ccc tcg tcg ctg ccc ctg tcc ctg ctg          102
281 Ser Gly Gln Val Arg Pro Leu Pro Ser Ser Leu Pro Leu Ser Leu Leu
282          10          15          20
284 ctg ctc ctc ctc ctg tgc tgc tcc ggc acc tcg tgg gga tgg agc acg          150
285 Leu Leu Leu Leu Leu Cys Cys Ser Gly Thr Ser Trp Gly Trp Ser Thr
286          25          30          35
288 tcc cgg gga gga gcc gcc agg gag tgc ggc ttc gat ggc aag ctg gag          198
289 Ser Arg Gly Gly Ala Ala Arg Glu Cys Gly Phe Asp Gly Lys Leu Glu
290          40          45          50          55
292 gcc ctg gag ccg cgc cac aag gtg cag tct gag gcc ggc tcc gtc cag          246
293 Ala Leu Glu Pro Arg His Lys Val Gln Ser Glu Ala Gly Ser Val Gln
294          60          65          70
296 tac ttc agc cgg ttc aac gaa gcc gac cgg gag ctc acc tgc gcc ggc          294
297 Tyr Phe Ser Arg Phe Asn Glu Ala Asp Arg Glu Leu Thr Cys Ala Gly

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/053,410

DATE: 02/12/2002

TIME: 12:00:33

Input Set : A:\1276SEQLIST.TXT

Output Set: N:\CRF3\02122002\J053410.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date